

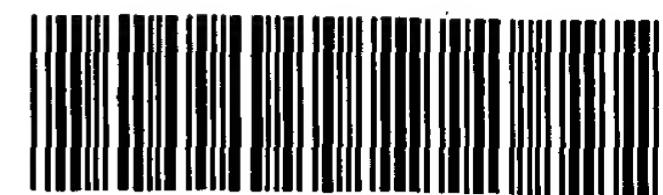
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1647

TECH CENTER 1600/2900



1600

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#10
Dmt
5-2-02

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/687,837

DATE: 04/23/2002 P.5
TIME: 09:34:13

Input Set : A:\20054210.app
Output Set: N:\CRF3\04232002\I687837.raw

3 <110> APPLICANT: Lu, Peter S.
4 Carman, Jonathan D.
5 Candia III, Albert F.
6 Arbbor Vita Corporation
8 <120> TITLE OF INVENTION: CLASP-2 TRANSMEMBRANE PROTEINS
10 <130> FILE REFERENCE: 020054-000210US
12 <140> CURRENT APPLICATION NUMBER: US 09/687,837
13 <141> CURRENT FILING DATE: 2000-10-13
15 <150> PRIOR APPLICATION NUMBER: US 60/129,171
16 <151> PRIOR FILING DATE: 1999-04-14
18 <150> PRIOR APPLICATION NUMBER: US 60/134,114
19 <151> PRIOR FILING DATE: 1999-05-14
21 <150> PRIOR APPLICATION NUMBER: US 60/134,118
22 <151> PRIOR FILING DATE: 1999-05-14
24 <150> PRIOR APPLICATION NUMBER: US 60/160,860
25 <151> PRIOR FILING DATE: 1999-10-21
27 <150> PRIOR APPLICATION NUMBER: US 60/162,498
28 <151> PRIOR FILING DATE: 1999-10-29
30 <150> PRIOR APPLICATION NUMBER: US 60/170,453
31 <151> PRIOR FILING DATE: 1999-12-13
33 <150> PRIOR APPLICATION NUMBER: US 60/176,195
34 <151> PRIOR FILING DATE: 2000-01-14
36 <150> PRIOR APPLICATION NUMBER: US 60/182,296
37 <151> PRIOR FILING DATE: 2000-02-14
39 <150> PRIOR APPLICATION NUMBER: US 09/547,276
40 <151> PRIOR FILING DATE: 2000-04-11
42 <150> PRIOR APPLICATION NUMBER: US 60/134,117
43 <151> PRIOR FILING DATE: 1999-05-14
45 <160> NUMBER OF SEQ ID NOS: 152
47 <170> SOFTWARE: PatentIn Ver. 2.1
49 <210> SEQ ID NO: 1
50 <211> LENGTH: 4807
51 <212> TYPE: DNA
52 <213> ORGANISM: Homo sapiens
54 <220> FEATURE:
55 <221> NAME/KEY: CDS
56 <222> LOCATION: (2)..(4060)
58 <220> FEATURE:
59 <223> OTHER INFORMATION: Human cadherin-like asymmetry protein 2A
60 (CLASP-2A)
62 <400> SEQUENCE: 1
63 a gtt tta cac cat cac caa aac cca gaa ttt tat gat gag att aaa ata 49
64 Val Leu His His Gln Asn Pro Glu Phe Tyr Asp Glu Ile Lys Ile

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65	1	5	10	15	
67	gag ttg ccc act cag ctg cat gaa aag cac cac ctg ttg ctc aca ttc				97
68	Glu Leu Pro Thr Gln Leu His Glu Lys His His Leu Leu Leu Thr Phe				
69	20	25	30		
71	tcc cat gtc agc tgt gac aac tca agt aaa gga agc acg aag aag agg				145
72	Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly Ser Thr Lys Lys Arg				
73	35	40	45		
75	gat gtc gtt gaa acc caa gtt ggc tac tcc tgg ctt ccc ctc ctg aaa				193
76	Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp Leu Pro Leu Leu Lys				
77	50	55	60		
79	gac gga agg gtg gtg aca agc gag cag cac atc ccg gtc tcg gcg aac				241
80	Asp Gly Arg Val Val Thr Ser Glu Gln His Ile Pro Val Ser Ala Asn				
81	65	70	75	80	
83	ctt cct tcg ggc tat ctt ggc tac caa gag ctt ggg atg ggc agg cat				289
84	Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu Gly Met Gly Arg His				
85	85	90	95		
87	tat ggt ccg gaa att aaa tgg gta gat gga ggc aag cca ctg ctg aaa				337
88	Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly Lys Pro Leu Leu Lys				
89	100	105	110		
91	att tcc act cat ctg gtt tct aca gtg tat act cag gat cag cat tta				385
92	Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr Gln Asp Gln His Leu				
93	115	120	125		
95	cat aat ttt ttc cag tac tgt cag aaa acc gaa tct gga gcc caa gcc				433
96	His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu Ser Gly Ala Gln Ala				
97	130	135	140		
99	tta gga aac gaa ctt gta aag tac ctt aag agt ctg cat gcg atg gaa				481
100	Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser Leu His Ala Met Glu				
101	145	150	155	160	
103	ggc cac gtg atg atc gcc ttc ttg ccc act atc cta aac cag ctg ttc				529
104	Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn Gln Leu Phe				
105	165	170	175		
107	cga gtc ctc acc aga gcc aca cag gaa gaa gtc gcg gtt aac gtg act				577
108	Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val Asn Val Thr				
109	180	185	190		
111	cgg gtc att att cat gtg gtt gcc cag tgc cat gag gaa gga ttg gag				625
112	Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu Gly Leu Glu				
113	195	200	205		
115	agc cac ttg agg tca tat gtt aag tac gcg tat aag gct gag cca tat				673
116	Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr				
117	210	215	220		
119	gtt gcc tct gaa tac aag aca gtg cat gaa gaa ctg acc aaa tcc atg				721
120	Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr Lys Ser Met				
121	225	230	235	240	
123	acc acg att ctc aag cct tct gcc gat ttc ctc acc agc aac aaa cta				769
124	Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser Asn Lys Leu				
125	245	250	255		
127	ctg agg tac tca tgg ttt ttc ttt gat gta ctg atc aaa tct atg gct				817
128	Leu Arg Tyr Ser Trp Phe Phe Asp Val Leu Ile Lys Ser Met Ala				
129	260	265	270		

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132	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	Leu	Arg	Asn	Gln	Arg	
133			275					280				285					
135	ttt	cct	gca	tcc	tat	cat	cat	gca	gcg	gaa	acc	gtt	gta	aat	atg	ctg	913
136	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val	Val	Asn	Met	Leu	
137			290					295				300					
139	atg	cca	cac	atc	act	cag	aag	ttt	gga	gat	aat	cca	gag	gca	tct	aag	961
140	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro	Glu	Ala	Ser	Lys	
141	305			310					315			320					
143	aac	gcg	aat	cat	agc	ctt	gct	gtc	ttc	atc	aag	aga	tgt	ttc	acc	ttc	1009
144	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg	Cys	Phe	Thr	Phe	
145			325					330				335					
147	atg	gac	agg	ggc	ttt	gtc	ttc	aag	cag	atc	aac	aac	tac	att	agc	tgt	1057
148	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn	Tyr	Ile	Ser	Cys	
149		340			345			350									
151	ttt	gct	cct	gga	gac	cca	aag	acc	ctc	ttt	gaa	tac	aag	ttt	gaa	ttt	1105
152	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	Tyr	Lys	Phe	Glu	Phe	
153		355			360			365									
155	ctc	cgt	gta	gtg	tgc	aac	cat	gaa	cat	tat	att	ccg	ttg	aac	tta	cca	1153
156	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	Pro	Leu	Asn	Leu	Pro	
157		370			375			380									
159	atg	cca	ttt	gga	aaa	ggc	agg	att	caa	aga	tac	caa	gac	ctc	cag	ctt	1201
160	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	Gln	Asp	Leu	Gln	Leu	
161	385		390			395			400								
163	gac	tac	tca	tta	aca	gat	gag	ttc	tgc	aga	aac	cac	ttc	ttg	gtg	gga	1249
164	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	His	Phe	Leu	Val	Gly	
165		405			410			415									
167	ctg	tta	ctg	agg	gag	gtg	ggg	aca	gcc	ctc	cag	gag	ttc	cg	gag	gtc	1297
168	Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	Glu	Phe	Arg	Glu	Val	
169		420			425			430									
171	cgt	ctg	atc	gcc	atc	agt	gtg	ctc	aag	aac	ctg	ctg	ata	aag	cat	tct	1345
172	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	Leu	Ile	Lys	His	Ser	
173		435			440			445									
175	ttt	gat	gac	aga	tat	gct	tca	agg	agc	cat	cag	gca	agg	ata	gcc	acc	1393
176	Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln	Ala	Arg	Ile	Ala	Thr	
177		450			455			460									
179	ctc	tac	ctg	cct	ctg	ttt	ggt	ctg	ctg	att	gaa	aac	gtc	cag	cg	atc	1441
180	Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu	Asn	Val	Gln	Arg	Ile	
181	465		470			475			480								
183	aat	gtg	agg	gat	gtg	tca	ccc	ttc	cct	gtg	aac	gcg	ggc	atg	acc	gtg	1489
184	Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn	Ala	Gly	Met	Thr	Val	
185		485			490			495									
187	aag	gat	gaa	tcc	ctg	gct	cta	cca	gct	gtg	aat	ccg	ctg	gtg	acg	ccg	1537
188	Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn	Pro	Leu	Val	Thr	Pro	
189		500			505			510									
191	cag	aag	gga	agc	acc	ctg	gac	aac	agc	ctg	cac	aag	gac	ctg	ctg	ggc	1585
192	Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	Lys	Asp	Leu	Leu	Gly	
193		515			520			525									
195	gcc	atc	tcc	ggc	att	gct	tct	cca	tat	aca	acc	tca	act	cca	aac	atc	1633

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196	Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Ser	Thr	Pro	Asn	Ile		
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199	aac	agt	gtg	aga	aat	gct	gat	tcg	aga	gga	tct	ctc	ata	agc	aca	gat	1681
200	Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser	Leu	Ile	Ser	Thr	Asp	
201	545					550					555					560	
203	tcg	ggt	aac	agc	ctt	cca	gaa	agg	aat	agt	gag	aag	agc	aat	tcc	ctg	1729
204	Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu	Lys	Ser	Asn	Ser	Leu	
205					565					570					575		
207	gat	aag	cac	caa	caa	agt	agc	aca	ttg	gga	aat	tcc	gtg	gtt	cgc	tgt	1777
208	Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn	Ser	Val	Val	Arg	Cys	
209					580				585			590					
211	gat	aaa	ctt	gac	cag	tct	gag	att	aag	agc	cta	ctg	atg	tgt	ttc	ctc	1825
212	Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu	Leu	Met	Cys	Phe	Leu	
213					595				600			605					
215	tac	atc	tta	aag	agc	atg	tct	gat	gat	gct	ttg	ttt	aca	tat	tgg	aac	1873
216	Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu	Phe	Thr	Tyr	Trp	Asn	
217					610				615			620					
219	aag	gct	tca	aca	tct	gaa	ctt	atg	gat	ttt	ttt	aca	ata	tct	gaa	gtc	1921
220	Lys	Ala	Ser	Thr	Ser	Glu	Leu	Met	Asp	Phe	Phe	Thr	Ile	Ser	Glu	Val	
221					625			630			635			640			
223	tgc	ctg	cac	cag	ttc	cag	tac	atg	ggg	aag	cga	tac	ata	gcc	agg	aac	1969
224	Cys	Leu	His	Gln	Phe	Gln	Tyr	Met	Gly	Lys	Arg	Tyr	Ile	Ala	Arg	Asn	
225					645				650			655					
227	cag	gag	ggg	ttg	gga	ccc	ata	gtt	cat	gat	cga	aag	tct	cag	aca	ttg	2017
228	Gln	Glu	Gly	Leu	Gly	Pro	Ile	Val	His	Asp	Arg	Lys	Ser	Gln	Thr	Leu	
229					660				665			670					
231	cct	gtt	tcc	cgt	aac	aga	aca	gga	atg	atg	cat	gcc	aga	ttg	cag	cag	2065
232	Pro	Val	Ser	Arg	Asn	Arg	Thr	Gly	Met	Met	His	Ala	Arg	Leu	Gln	Gln	
233					675				680			685					
235	ctg	ggc	agc	ctg	gat	aac	tct	ctc	act	ttt	aac	cac	agc	tat	ggc	cac	2113
236	Leu	Gly	Ser	Leu	Asp	Asn	Ser	Leu	Thr	Phe	Asn	His	Ser	Tyr	Gly	His	
237					690			695			700						
239	tcg	gac	gca	gat	gtt	ctg	cac	cag	tca	tta	ctt	gaa	gcc	aac	att	gct	2161
240	Ser	Asp	Ala	Asp	Val	Leu	His	Gln	Ser	Leu	Leu	Glu	Ala	Asn	Ile	Ala	
241					705			710			715			720			
243	act	gag	gtt	tgc	aca	gct	ctg	gac	acg	ctt	tct	cta	ttt	aca	ttg		2209
244	Thr	Glu	Val	Cys	Leu	Thr	Ala	Leu	Asp	Thr	Leu	Ser	Leu	Phe	Thr	Leu	
245					725				730			735					
247	gcg	ttt	aag	aac	cag	ctc	ctg	gcc	gac	cat	gga	cat	aat	cct	ctc	atg	2257
248	Ala	Phe	Lys	Asn	Gln	Leu	Leu	Ala	Asp	His	Gly	His	Asn	Pro	Leu	Met	
249					740				745			750					
251	aaa	aaa	gtt	ttt	gat	gtc	tac	ctg	tgt	ttt	ctt	caa	aaa	cat	cag	tct	2305
252	Lys	Lys	Val	Phe	Asp	Val	Tyr	Leu	Cys	Phe	Leu	Gln	Lys	His	Gln	Ser	
253					755				760			765					
255	gaa	acg	gct	tta	aaa	aat	gtc	ttc	act	gcc	tta	agg	tcc	tta	att	tat	2353
256	Glu	Thr	Ala	Leu	Lys	Asn	Val	Phe	Thr	Ala	Leu	Arg	Ser	Leu	Ile	Tyr	
257					770			775			780						
259	aag	ttt	ccc	tca	aca	ttc	tat	gaa	ggg	aga	gca	gac	atg	tgt	gcg	gct	2401
260	Lys	Phe	Pro	Ser	Thr	Phe	Tyr	Glu	Gly	Arg	Ala	Asp	Met	Cys	Ala	Ala	

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263	ctg	tgt tac gag att ctc aag tgc tgt aac tcc aag ctg agc tcc atc		2449	
264	Leu	Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile			
265		805	810	815	
267	agg acg gag gcc tcc cag ctg ctc tac ttc ctg atg agg aac aac ttt			2497	
268	Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe				
269		820	825	830	
271	gat tac act gga aag aag tcc ttt gtc cg ^g aca cat ttg caa gtc atc			2545	
272	Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile				
273		835	840	845	
275	ata tct gtc agc cag ctg ata gca gac gtt gtt ggc att ggg gaa acc			2593	
276	Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Glu Thr				
277		850	855	860	
279	aga ttc cag cag tcc ctg tcc atc atc aac aac tgt gcc aac agt gac			2641	
280	Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp				
281		865	870	875	880
283	cgg ctt att aag cac acc agc ttc tcc tct gat gtg aag gac tta acc			2689	
284	Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr				
285		885	890	895	
287	aaa agg ata cgc acg gtg cta atg gcc acc gcc cag atg aag gag cat			2737	
288	Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His				
289		900	905	910	
291	gag aac gac cca gag atg ctg gtg gac ctc cag tac agc ctg gcc aaa			2785	
292	Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys				
293		915	920	925	
295	tcc tat gcc agc acg ccc gag ctc agg aag acg tgg ctc gac agc atg			2833	
296	Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met				
297		930	935	940	
299	gcc agg atc cat gtc aaa aat ggc gat ctc tca gag gca gca atg tgc			2881	
300	Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys				
301		945	950	955	960
303	tat gtc cac gta aca gcc cta gtg gca gaa tat ctc aca cgg aaa ggc			2929	
304	Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Gly				
305		965	970	975	
307	gtg ttt aga caa gga tgc acc gcc ttc agg gtc att acc cca aac atc			2977	
308	Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro Asn Ile				
309		980	985	990	
311	gac gag gag gcc tcc atg atg gaa gac gtg ggg atg cag gat gtc cat			3025	
312	Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp Val His				
313		995	1000	1005	
315	tcc aac gag gat gtg ctg atg gag ctc ctt gag cag tgc gca gat gga			3073	
316	Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp Gly				
317		1010	1015	1020	
319	ctc tgg aaa gcc gag cgc tac gag ctc atc gcc gac atc tac aaa ctt			3121	
320	Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu				
321		1025	1030	1035	1040
323	atc atc ccc att tat gag aag cgg agg gat ttc ttt gaa gat gaa gat			3169	
324	Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe Glu Asp Glu Asp				
325		1045	1050	1055	

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
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Input Set : A:\20054210.app
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L:5207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
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L:5229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69
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L:5262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
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L:5275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71
L:5305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71
L:5330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:5332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:5333 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:5334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:5335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:5336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:5364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:5366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:5392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:5393 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:5394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:5395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:5396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:5421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:5423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:5424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/687,837

DATE: 04/23/2002
TIME: 09:34:14

Input Set : A:\20054210.app
Output Set: N:\CRF3\04232002\I687837.raw

L:5425 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:5451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76